WEST Search History

Hide Items | Restore | Clear | Cancel

DATE: Monday, April 25, 2005

Hide?	Set Name	Query	Hit Count
		DB=PGPB,USPT,EPAB; PLUR=YES; OP=ADJ	
☐	L12	L11 AND L9	65
☐	L11	L10 AND L3	.261
☐	L10	l2 AND L1	997
☐	L9	L8 or l7	26517
☐	L8	(435/7.1,7.23)![CCLS]	11848
☐	L7	(530/350)![CCLS]	16625
☐	L6	(530)![CCLS]	0
☐	L5	(530)![CCLS]	0
☐	L4	84P2A9	0
☐	L3	prostate	33051
☐	L2	tumor$ or tumuor$ or cancer$ or neoplas$	161183
☐	L1	(jakobovits or afar or challita$ or levin or mitchell or hubert).in.	32792

END OF SEARCH HISTORY

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 3, 2005, 05:44:40 ; Search time 174.5 Seconds
                                           (without alignments)
                                           10394.878 Million cell updates/sec

Title: US-09-771-312-1
Perfect score: 4167
Sequence: 1 attcggcacgaggtggaagt..........accaaaaaaaaaaaaaaaaa 2345

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103618_22701/app_query.fasta_1.2
503
-DB=A_Geneseq_16Dec04 -QFMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09771312_@CGN_1_1_242_@runat_01042005_103618_22701 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   A_Geneseq_16Dec04:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*

         Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2826	67.8	528	4	AAB92632	Aab92632 Human pro
2	2826	67.8	528	5	ABB97288	Abb97288 Novel hum
3	2694	64.7	504	4	AAU06524	Aau06524 Prostate
4	1940	46.6	376	8	ADR99239	Adr99239 Hypotheti
5	1202	28.8	313	4	ABG08002	Abg08002 Novel hum
6	608.5	14.6	423	4	ABG23408	Abg23408 Novel hum
7	591.5	14.2	446	5	ABB75706	Abb75706 Human pho
8	588.5	14.1	482	5	ABP43772	Abp43772 14 clone
9	533.5	12.8	453	5	ABB97561	Abb97561 Novel hum
10	530.5	12.7	351	4	AAB94662	Aab94662 Human pro
11	530.5	12.7	351	5	ABB97470	Abb97470 Novel hum
12	338	8.1	275	4	AAB92468	Aab92468 Human pro
13	320.5	7.7	223	4	AAM15386	Aam15386 Peptide #
14	320.5	7.7	223	4	ABB34392	Abb34392 Peptide #
15	320.5	7.7	223	4	AAM27874	Aam27874 Peptide #
16	320.5	7.7	223	4	ABB29229	Abb29229 Peptide #
17	320.5	7.7	223	4	AAM67577	Aam67577 Human bon
18	320.5	7.7	223	4	AAM55182	Aam55182 Human bra
19	320.5	7.7	223	4	ABG49223	Abg49223 Human liv
20	320.5	7.7	223	4	AAM03148	Aam03148 Peptide #
21	320.5	7.7	223	5	ABG37168	Abg37168 Human pep
22	320.5	7.7	223	8	ABO59933	Abo59933 Human gen
23	236.5	5.7	123	4	AAM95677	Aam95677 Human rep
24	198	4.8	1038	7	ADC03412	Adc03412 Rice flow
25	169.5	4.1	554	3	AAG36165	Aag36165 Arabidops
26	169.5	4.1	652	3	AAG36164	Aag36164 Arabidops
27	169.5	4.1	781	3	AAG36163	Aag36163 Arabidops
28	169	4.1	767	6	ABR53431	Abr53431 Protein s
29	169	4.1	767	7	ADK64670	Adk64670 Disease t
30	162.5	3.9	815	5	AAG78388	Aag78388 Human H37
31	162.5	3.9	815	7	AAE38620	Aae38620 Human H37
32	162.5	3.9	815	7	AAE38621	Aae38621 Human H37
33	162.5	3.9	815	8	ADP23184	Adp23184 PRO polyp
34	162	3.9	381	2	AAY07056	Aay07056 Renal can
35	159.5	3.8	573	4	ADM19760	Adm19760 Protein e
36	158.5	3.8	962	4	ABG04842	Abg04842 Novel hum
37	158.5	3.8	1403	8	ADH09502	Adh09502 Human hos
38	158.5	3.8	1462	6	ABP58346	Abp58346 Human cel
39	158.5	3.8	1462	6	ABU05132	Abu05132 Human exp
40	158.5	3.8	1462	6	ABU05136	Abu05136 Human exp
41	158.5	3.8	1462	6	ABU05131	Abu05131 Human exp
42	158.5	3.8	1462	6	ABU05135	Abu05135 Human exp
43	158.5	3.8	1462	7	ADJ68950	Adj68950 Human hea
44	158.5	3.8	1462	8	ADH09503	Adh09503 Human hos
45	158.5	3.8	1462	8	ADP55142	Adp55142 Human PRO

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 3, 2005, 08:28:10 ; Search time 37.5 Seconds
                                             (without alignments)
                                             9336.110 Million cell updates/sec

Title: US-09-771-312-1
Perfect score: 4167
Sequence: 1 attcggcacgaggtggaagt.........accaaaaaaaaaaaaaaaaa 2345

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103620_22743/app_query.fasta_1.2
503
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=rai -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09771312_@CGN_1_1_46_@runat_01042005_103620_22743 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_AA:*
                 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
        %

Result No.	Score	Query Match	Length	DB	ID	Description
1	666	16.0	124	4	US-09-621-976-4580	Sequence 4580, Ap
2	162.5	3.9	815	4	US-09-538-092-1196	Sequence 1196, Ap
3	158.5	3.8	1462	4	US-09-538-092-1043	Sequence 1043, Ap
4	156	3.7	929	4	US-09-538-092-1232	Sequence 1232, Ap
5	154.5	3.7	620	4	US-09-270-767-46214	Sequence 46214, A
6	147.5	3.5	362	4	US-09-270-767-42306	Sequence 42306, A
7	139	3.3	788	3	US-08-630-915A-30	Sequence 30, Appl
8	139	3.3	788	4	US-09-879-957-30	Sequence 30, Appl
9	133.5	3.2	1564	4	US-10-144-198-2	Sequence 2, Appli
10	133.5	3.2	1564	4	US-10-144-198-4	Sequence 4, Appli
11	133	3.2	664	1	US-08-421-661-6	Sequence 6, Appli
12	129	3.1	1034	4	US-09-976-594-590	Sequence 590, App
13	127.5	3.1	748	3	US-08-725-459B-24	Sequence 24, Appl
14	127	3.0	709	4	US-09-949-016-10367	Sequence 10367, A
15	126.5	3.0	1402	4	US-09-248-796A-14503	Sequence 14503, A
16	126	3.0	598	4	US-09-538-092-1083	Sequence 1083, Ap
17	126	3.0	664	4	US-09-917-254-78	Sequence 78, Appl
18	126	3.0	1400	4	US-09-764-176-7	Sequence 7, Appli
19	123	3.0	971	4	US-09-538-092-1332	Sequence 1332, Ap
20	122.5	2.9	621	4	US-09-248-796A-15807	Sequence 15807, A
21	122.5	2.9	976	3	US-09-302-812-4	Sequence 4, Appli
22	122.5	2.9	976	3	US-09-511-477-4	Sequence 4, Appli
23	122.5	2.9	976	3	US-09-511-507-4	Sequence 4, Appli
24	122	2.9	968	3	US-09-302-812-6	Sequence 6, Appli
25	122	2.9	968	3	US-09-511-477-6	Sequence 6, Appli
26	122	2.9	968	3	US-09-511-507-6	Sequence 6, Appli
27	121	2.9	733	3	US-08-725-459B-21	Sequence 21, Appl
28	121	2.9	769	3	US-08-725-459B-39	Sequence 39, Appl
29	120.5	2.9	1992	4	US-09-538-092-1327	Sequence 1327, Ap
30	120	2.9	769	3	US-08-725-459B-37	Sequence 37, Appl
31	120	2.9	769	3	US-08-725-459B-38	Sequence 38, Appl
32	120	2.9	769	3	US-08-725-459B-40	Sequence 40, Appl
33	120	2.9	1739	4	US-09-976-594-76	Sequence 76, Appl
34	120	2.9	1739	4	US-09-538-092-824	Sequence 824, App
35	120	2.9	1740	4	US-09-949-016-8860	Sequence 8860, Ap
36	119.5	2.9	1589	4	US-09-543-681A-4998	Sequence 4998, Ap
37	119.5	2.9	2842	1	US-07-741-940-7	Sequence 7, Appli
38	119.5	2.9	2842	1	US-08-289-548A-7	Sequence 7, Appli
39	119.5	2.9	2842	1	US-08-452-654-7	Sequence 7, Appli
40	119.5	2.9	2842	4	US-08-449-731-7	Sequence 7, Appli
41	119.5	2.9	2843	1	US-07-741-940-2	Sequence 2, Appli
42	119.5	2.9	2843	1	US-08-289-548A-2	Sequence 2, Appli
43	119.5	2.9	2843	1	US-08-452-654-2	Sequence 2, Appli
44	119.5	2.9	2843	1	US-08-452-655B-2	Sequence 2, Appli
45	119.5	2.9	2843	1	US-08-452-655B-7	Sequence 7, Appli

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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 3, 2005, 09:03:56 ; Search time 149 Seconds

Title: US-09-771-312-1
Perfect score: 4167
Sequence: 1 attcggcacgaggtggaagt.........accaaaaaaaaaaaaaaaaa 2345

Scoring table: BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop 6.0 , Fgapext 7.0
                  Delop   6.0 , Delext   7.0

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 2826744

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103621_22833/app_query.fasta_1.2
503
-DB=Published_Applications_AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09771312_@CGN_1_1_207_@runat_01042005_103621_22833
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_AA:*
                  1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                  2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                  3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                  4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                  5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                  6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                  7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                  8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                  9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
                  10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
                  11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
                  12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                  13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
                  14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
                  15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
                  16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
                  17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                  18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2694	64.7	504	11	US-09-771-312-2	Sequence 2, Appli
2	1940	46.6	376	16	US-10-788-792-245	Sequence 245, App
3	529	12.7	320	11	US-09-771-312-5	Sequence 5, Appli
4	320.5	7.7	223	9	US-09-864-761-42782	Sequence 42782, A
5	320.5	7.7	223	14	US-10-029-386-33567	Sequence 33567, A
6	236.5	5.7	123	10	US-09-764-891-4335	Sequence 4335, Ap
7	188	4.5	313	15	US-10-424-599-174584	Sequence 174584,
8	181.5	4.4	564	15	US-10-425-114-71576	Sequence 71576, A
9	173	4.2	776	16	US-10-437-963-198660	Sequence 198660,
10	162.5	3.9	815	10	US-09-957-763-2	Sequence 2, Appli
11	162.5	3.9	815	10	US-09-957-763-4	Sequence 4, Appli
12	160.5	3.9	729	16	US-10-437-963-127682	Sequence 127682,
13	158.5	3.8	1462	14	US-10-287-218-17	Sequence 17, Appl
14	158.5	3.8	1462	16	US-10-408-765A-756	Sequence 756, App
15	158.5	3.8	1462	16	US-10-474-291-17	Sequence 17, Appl
16	157.5	3.8	1604	16	US-10-437-963-123905	Sequence 123905,
17	155.5	3.7	150	16	US-10-767-701-33562	Sequence 33562, A
18	154.5	3.7	643	15	US-10-427-224-13	Sequence 13, Appl
19	153.5	3.7	668	15	US-10-424-599-256096	Sequence 256096,
20	151	3.6	641	9	US-09-925-298-652	Sequence 652, App
21	151	3.6	641	14	US-10-102-806-652	Sequence 652, App
22	148.5	3.6	1577	15	US-10-369-493-6924	Sequence 6924, Ap
23	148.5	3.6	1577	15	US-10-369-493-6925	Sequence 6925, Ap
24	148.5	3.6	1577	15	US-10-369-493-6926	Sequence 6926, Ap
25	142	3.4	2515	15	US-10-276-774-2651	Sequence 2651, Ap
26	140	3.4	198	15	US-10-108-260A-4770	Sequence 4770, Ap
27	139.5	3.3	158	16	US-10-767-701-42233	Sequence 42233, A
28	139	3.3	788	9	US-09-879-957-30	Sequence 30, Appl
29	139	3.3	788	16	US-10-807-856-30	Sequence 30, Appl
30	139	3.3	813	16	US-10-437-963-120203	Sequence 120203,
31	138	3.3	42	11	US-09-771-312-6	Sequence 6, Appli
32	138	3.3	557	9	US-09-764-856-60	Sequence 60, Appl
33	138	3.3	557	11	US-09-764-856-60	Sequence 60, Appl
34	138	3.3	557	14	US-10-102-627-60	Sequence 60, Appl
35	136	3.3	910	15	US-10-425-114-54499	Sequence 54499, A
36	136	3.3	1134	13	US-10-001-873-50	Sequence 50, Appl
37	135	3.2	3051	15	US-10-144-194A-62	Sequence 62, Appl
38	134	3.2	446	9	US-09-764-856-70	Sequence 70, Appl
39	134	3.2	446	11	US-09-764-856-70	Sequence 70, Appl
40	134	3.2	446	14	US-10-102-627-70	Sequence 70, Appl
41	134	3.2	644	16	US-10-437-963-109393	Sequence 109393,
42	133.5	3.2	1564	15	US-10-144-198-2	Sequence 2, Appli
43	133.5	3.2	1564	15	US-10-144-198-4	Sequence 4, Appli
44	131.5	3.2	324	15	US-10-425-114-59181	Sequence 59181, A
45	131.5	3.2	341	15	US-10-424-599-256098	Sequence 256098, -

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OM nucleic - protein search, using frame_plus_n2p model

Run on: April 3, 2005, 08:19:20 ; Search time 44.5 Seconds
                                           (without alignments)
                                           10140.598 Million cell updates/sec

Title: US-09-771-312-1
Perfect score: 4167
Sequence: 1 attcggcacgaggtggaagt..........accaaaaaaaaaaaaaaaaa 2345

Scoring table: BLOSUM62
                Xgapop 10.0 , Xgapext 0.5
                Ygapop 10.0 , Ygapext 0.5
                Fgapop 6.0 , Fgapext 7.0
                Delop   6.0 , Delext   7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103619_22728/app_query.fasta_1.2
503
-DB=PIR_79 -QFMT=fastan -SUFFIX=rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09771312_@CGN_1_1_60_@runat_01042005_103619_22728 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   PIR_79:*
                1: pir1:*
                2: pir2:*
                3: pir3:*
                4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	177.5	4.3	1105	2	T47582	hypothetical prote
2	169	4.1	767	2	S63182	hypothetical prote
3	158.5	3.8	1403	1	A47328	natural killer cel
4	156	3.7	542	2	T46464	hypothetical prote
5	155.5	3.7	695	2	T40168	hypothetical prote
6	154.5	3.7	643	2	A96636	unknown protein, 7
7	152	3.6	669	2	T28754	hypothetical prote
8	148.5	3.6	1577	2	T19722	hypothetical prote
9	146	3.5	368	2	G88636	protein W09G12.7 [
10	146	3.5	2152	2	T45583	hypothetical prote
11	145	3.5	3498	2	T22330	hypothetical prote
12	140.5	3.4	699	2	I38073	nucleolar phosphop
13	138	3.3	775	2	T21259	hypothetical prote
14	137.5	3.3	539	2	T15256	hypothetical prote
15	136.5	3.3	896	2	D96556	hypothetical prote
16	135	3.2	552	2	T27191	hypothetical prote
17	134.5	3.2	954	2	E86174	protein F19P19.26
18	133.5	3.2	1672	2	T46237	hypothetical prote
19	133	3.2	705	2	D88536	acidic protein - C
20	133	3.2	705	2	S27786	acidic protein - C
21	133	3.2	943	2	A42681	centromere protein
22	133	3.2	2526	2	T20531	hypothetical prote
23	133	3.2	2738	2	E88320	protein F07A11.6 [
24	132	3.2	679	2	S48437	hypothetical prote
25	131.5	3.2	425	2	S55147	hypothetical prote
26	131.5	3.2	1150	2	T13824	LK6 protein kinase
27	130	3.1	608	2	T02299	hypothetical prote
28	129.5	3.1	2722	2	T20532	hypothetical prote
29	129	3.1	817	2	S53919	hypothetical prote
30	128.5	3.1	543	2	T27190	hypothetical prote
31	128.5	3.1	845	2	A45669	neurofilament trip
32	128	3.1	664	2	S60062	hevin precursor -
33	128	3.1	816	2	T19049	hypothetical prote
34	127.5	3.1	493	2	T02376	hypothetical prote
35	127.5	3.1	677	1	S09078	chromogranin B pre
36	127	3.0	763	2	T08929	hypothetical prote
37	127	3.0	786	2	T33856	hypothetical prote
38	127	3.0	963	2	T04002	hypothetical prote
39	126.5	3.0	390	2	T34137	hypothetical prote
40	126	3.0	598	2	B40713	cylicin I - human
41	126	3.0	1032	2	A57514	RNA helicase HEL11
42	125.5	3.0	1560	2	T42727	proliferation pote
43	125.5	3.0	2218	2	B84683	hypothetical prote
44	125	3.0	1274	2	A89959	hypothetical prote
45	125	3.0	1877	2	T21861	hypothetical prote

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 3, 2005, 05:51:15 ; Search time 214 Seconds
                                            (without alignments)
                                            11222.670 Million cell updates/sec

Title: US-09-771-312-1
Perfect score: 4167
Sequence: 1 attcggcacgaggtggaagt.........accaaaaaaaaaaaaaaaaa 2345

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_n2p.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103619_22715/app_query.fasta_1.2
503
-DB=UniProt_03 -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09771312_@CGN_1_1_320_@runat_01042005_103619_22715 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :,   UniProt_03:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                     %
Result   Query
  No.   Score   Match Length DB ID   Description
----
     1   2826   67.8   528 1 GPT2_HUMAN   Q9nw75 homo sapien
     2 2394.5   57.5   527 1 GPT2_MOUSE   Q7tqc7 mus musculu
     3 1622.5   38.9   375 2 Q9D3E7   Q9d3e7 mus musculu

4	1595	38.3	410	2	Q6AY15	Q6ay15	rattus norv
5	1140	27.4	216	2	Q6PIX0	Q6pix0	homo sapien
6	636.5	15.3	500	2	Q6ZPW9	Q6zpw9	mus musculu
7	627.5	15.1	482	2	Q6PE65	Q6pe65	mus musculu
8	593.5	14.2	482	2	Q9H3M3	Q9h3m3	homo sapien
9	566	13.6	408	2	Q8CD08	Q8cd08	mus musculu
10	565	13.6	408	2	Q9DA49	Q9da49	mus musculu
11	533.5	12.8	453	2	Q9NWQ4	Q9nwq4	homo sapien
12	530.5	12.7	351	2	Q6PEJ7	Q6pej7	homo sapien
13	530.5	12.7	354	2	Q9ULR8	Q9ulr8	homo sapien
14	514.5	12.3	107	2	Q9CSX3	Q9csx3	mus musculu
15	338	8.1	275	2	Q9NWH0	Q9nwh0	homo sapien
16	320.5	7.7	221	2	Q9ULA8	Q9ula8	homo sapien
17	199	4.8	928	2	Q6H4V9	Q6h4v9	oryza sativ
18	177.5	4.3	812	2	Q6C233	Q6c233	yarrowia li
19	177.5	4.3	1007	2	Q8VYR8	Q8vyr8	arabidopsis
20	177.5	4.3	1105	2	Q9M383	Q9m383	arabidopsis
21	173	4.2	663	2	Q80UY8	Q80uy8	mus musculu
22	173	4.2	742	2	Q6Z2C8	Q6z2c8	oryza sativ
23	172	4.1	1067	2	Q8BY32	Q8by32	m mus muscu
24	171	4.1	1067	2	Q8CH09	Q8ch09	mus musculu
25	169.5	4.1	781	2	Q9SF87	Q9sf87	arabidopsis
26	169	4.1	767	1	YNW4_YEAST	P53866	saccharomyc
27	167	4.0	470	2	Q8CFM0	Q8cfm0	mus musculu
28	162.5	3.9	749	2	Q6DDU9	Q6ddu9	xenopus lae
29	162.5	3.9	815	1	RBM5_HUMAN	P52756	homo sapien
30	162	3.9	520	2	Q99KV9	Q99kv9	mus musculu
31	162	3.9	815	2	Q91YE7	Q91ye7	mus musculu
32	158.5	3.8	1462	1	NKCR_HUMAN	P30414	homo sapien
33	158	3.8	1191	2	Q9XYY3	Q9xyy3	dictyosteli
34	157.5	3.8	808	2	Q6BYP9	Q6byp9	debaryomyce
35	157.5	3.8	852	1	RBMA_RAT	P70501	rattus norv
36	157.5	3.8	853	2	Q8BTP8	Q8btp8	mus musculu
37	157.5	3.8	857	2	Q80U75	Q80u75	mus musculu
38	157.5	3.8	930	2	Q99KG3	Q99kg3	mus musculu
39	156.5	3.8	1208	2	Q7PNP6	Q7pnp6	anopheles g
40	156	3.7	542	2	Q9NTB1	Q9ntb1	homo sapien
41	156	3.7	852	2	Q9BTX0	Q9btx0	homo sapien
42	156	3.7	929	1	RBMA_HUMAN	P98175	homo sapien
43	156	3.7	930	2	Q9BTE4	Q9bte4	homo sapien
44	156	3.7	995	2	Q7Z3D7	Q7z3d7	homo sapien
45	155.5	3.7	695	2	O74363	O74363	schizosacch

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OM nucleic - nucleic search, using sw model

Run on: April 2, 2005, 23:06:48 ; Search time 10037 Seconds
                                            (without alignments)
                                            11320.861 Million cell updates/sec

Title: US-09-771-312-1
Perfect score: 2345
Sequence: 1 attcggcacgaggtggaagt..........accaaaaaaaaaaaaaaaaa 2345

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                               SUMMARIES

               %
Result   Query
   No.   Score Match Length DB ID   Description
   ----
       1   2345 100.0 2345   6 AX206855   AX206855 Sequence
       2 2319.2 98.9 2344   6 AX405697   AX405697 Sequence
       3 2314.4 98.7 2338   6 BD155908   BD155908 Primer fo

	4	2314.4	98.7	2338	6	AX876032	AX876032	Sequence
	5	2314.4	98.7	2338	9	AK001114	AK001114	Homo sapi
	6	1269	54.1	4537	10	BC054810	BC054810	Mus muscu
	7	1176	50.1	4022	6	BD183390	BD183390	Novel gen
	8	1172.8	50.0	3250	9	BC063474	BC063474	Homo sapi
	9	1145.4	48.8	3189	9	BC042193	BC042193	Homo sapi
	10	1026	43.8	1026	6	CQ720787	CQ720787	Sequence
	11	1008.2	43.0	1021	9	AK024701	AK024701	Homo sapi
c	12	878	37.4	177654	2	AC025988	AC025988	Homo sapi
c	13	878	37.4	185148	9	AC096641	AC096641	Homo sapi
c	14	874.8	37.3	178229	2	AC009420	AC009420	Homo sapi
	15	756.2	32.2	817	6	BD146304	BD146304	Primer fo
	16	756.2	32.2	817	6	AX866242	AX866242	Sequence
c	17	718.6	30.6	135060	9	AL354659	AL354659	Human DNA
c	18	718.6	30.6	142908	2	AL513172	AL513172	Homo sapi
	19	713.8	30.4	759	9	BC027719	BC027719	Homo sapi
	20	686.8	29.3	1392	10	BC079232	BC079232	Rattus no
	21	527.6	22.5	180315	10	AC107843	AC107843	Mus muscu
c	22	527.6	22.5	260404	10	AC110033	AC110033	Mus muscu
c	23	488	20.8	530	6	BD151813	BD151813	Primer fo
c	24	488	20.8	530	6	AX871751	AX871751	Sequence
	25	488	20.8	254644	2	AC136836	AC136836	Rattus no
	26	488	20.8	256511	2	AC135040	AC135040	Rattus no
c	27	488	20.8	262721	2	AC106265	AC106265	Rattus no
	28	467	19.9	467	6	CQ683049	CQ683049	Sequence
	29	448.4	19.1	469	6	AR413083	AR413083	Sequence
	30	448.4	19.1	469	6	AX969917	AX969917	Sequence
	31	448.4	19.1	469	6	BD108636	BD108636	EST and e
c	32	405.2	17.3	425	6	AX206857	AX206857	Sequence
	33	386.4	16.5	445	6	CQ431223	CQ431223	Sequence
	34	361.4	15.4	448	6	CQ422360	CQ422360	Sequence
	35	348.2	14.8	64462	2	AC107950	AC107950	Homo sapi
	36	316.8	13.5	407	6	CQ735676	CQ735676	Sequence
c	37	291.2	12.4	360	6	AX409847	AX409847	Sequence
	38	216	9.2	66626	2	AC100660	AC100660	Mus muscu
c	39	216	9.2	202785	10	AC108796	AC108796	Mus muscu
	40	191.8	8.2	308	6	CQ673353	CQ673353	Sequence
	41	188.6	8.0	201	11	BV202345	BV202345	sqnm20884
	42	181.2	7.7	208	6	BD058539	BD058539	Secreted
c	43	170	7.2	148801	5	BX004824	BX004824	Zebrafish
c	44	170	7.2	149784	2	BX005303	BX005303	Danio rer
c	45	163.6	7.0	69478	2	AC101461	AC101461	Mus muscu

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OM nucleic - nucleic search, using sw model

Run on: April 2, 2005, 21:36:18 ; Search time 1237 Seconds
                                           (without alignments)
                                           11222.145 Million cell updates/sec

Title: US-09-771-312-1
Perfect score: 2345

Sequence: .1 attcggcacgaggtggaagt..........accaaaaaaaaaaaaaaaaa 2345

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_16Dec04:*
                  1: geneseqn1980s:*
                  2: geneseqn1990s:*
                  3: geneseqn2000s:*
                  4: geneseqn2001as:*
                  5: geneseqn2001bs:*
                  6: geneseqn2002as:*
                  7: geneseqn2002bs:*
                  8: geneseqn2003as:*
                  9: geneseqn2003bs:*
                  10: geneseqn2003cs:*
                  11: geneseqn2003ds:*
                  12: geneseqn2004as:*
                  13: geneseqn2004bs:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                      %
Result   Query
   No.   Score Match Length DB   ID   Description
     ----
       1   2345 100.0   2345   5   AAS11663   Aas11663 Prostate
       2 2319.2   98.9   2344   6   ABN59701   Abn59701 Novel hum
       3 2314.8   98.7   2583 11   ACN91982   Acn91982 Breast ca
       4 2314.4   98.7   2338   4   AAH13916   Aah13916 Human cDN
       5 2314.4   98.7   2338 13   ADR99112   Adr99112 Hypotheti
       6   756.2   32.2   817   4   AAH04312   Aah04312 Human cDN
       7   726   31.0   1563   5   AAS72189   Aas72189 DNA encod
   c   8   549.8   23.4   553   6   ABT10667   Abt10667 Human bre
   c   9   488   20.8   530   4   AAH09821   Aah09821 Human cDN
   c 10   405.2   17.3   425   5   AAS11664   Aas11664 84P2A9 su
      11   386.4   16.5   445   4   AAL23787   Aal23787 Human bre
      12   385.4   16.4   492 11   ACN84952   Acn84952 Breast ca
      13   382   16.3   382   6   ABK35967   Abk35967 cDNA sequ
      14   361.4   15.4   448   4   AAL14929   Aal14929 Human bre
   c 15   291.2   12.4   360   6   ABN95996   Abn95996 Gene #249
      16   250.2   10.7   330   7   ADS72558   Ads72558 Human kid
      17   181.2   7.7   208   2   AAV86416   Aav86416 EST clone

18	121	5.2	1823	6	ABL53700	Abl53700 Human pho
19	121	5.2	2433	6	ABQ61016	Abq61016 14 clone
20	118.4	5.0	2434	6	ABN59974	Abn59974 Novel hum
21	116	4.9	1474	6	ABN59883	Abn59883 Novel hum
22	115.4	4.9	2112	4	AAH16534	Aah16534 Human cDN
23	113	4.8	1656	5	AAS87595	Aas87595 DNA encod
24	109.8	4.7	740	4	AAH03286	Aah03286 Human cDN
25	109.8	4.7	1851	4	AAH13673	Aah13673 Human cDN
26	99.8	4.3	371	4	AAL01647	Aal01647 Human rep
27	87	3.7	109	3	AAC12727	Aac12727 Human sec
28	85.4	3.6	747	2	AAZ16358	Aaz16358 Human gen
29	82	3.5	300	2	AAZ14849	Aaz14849 Human gen
30	64.8	2.8	321	5	ADL36721	Adl36721 Human ova
31	64.8	2.8	321	5	ADI71565	Adi71565 Human ova
32	64.8	2.8	390	5	ADL43105	Adl43105 Human ova
33	60	2.6	60	6	ABN33768	Abn33768 Human spl
34	57.8	2.5	673	4	AAI21087	Aai21087 Probe #11
35	57.8	2.5	673	4	ABA66165	Aba66165 Human foe
36	57.8	2.5	673	4	AAI46350	Aai46350 Probe #15
37	57.8	2.5	673	4	ABA48281	Aba48281 Human bre
38	57.8	2.5	673	4	AAK40330	Aak40330 Human bon
39	57.8	2.5	673	4	AAK14584	Aak14584 Human bra
40	57.8	2.5	673	4	ABS39901	Abs39901 Human liv
41	57.8	2.5	673	5	AAI06807	Aai06807 Probe #67
42	57.8	2.5	673	6	ABS14348	Abs14348 Human gen
43	57.8	2.5	673	12	ACH91528	Ach91528 Human gen
44	57.8	2.5	978	4	AAI11878	Aai11878 Probe #18
45	57.8	2.5	978	4	ABA53579	Aba53579 Human foe

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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 00:18:03 ; Search time 394 Seconds
                                          (without alignments)
                                          9738.754 Million cell updates/sec

Title: US-09-771-312-1
Perfect score: 2345
Sequence: 1 attcggcacgaggtggaagt..........accaaaaaaaaaaaaaaaaa 2345

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

```
Database :          Issued_Patents_NA:*
                 1:  /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2:  /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3:  /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4:  /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5:  /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                 6:  /cgn2_6/ptodata/1/ina/backfiles1.seq:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.


                                  SUMMARIES
                          %
Result                 Query
     No.     Score     Match  Length  DB   ID                     Description
     --------------------------------------------------------------------------
       1     448.4      19.1     469   4   US-09-621-976-720       Sequence 720, App
       2        87       3.7     109   4   US-09-513-999C-16802    Sequence 16802, A
c      3        78       3.3    7218   1   US-08-232-463-14        Sequence 14, Appl
c      4      47.2       2.0    1141   4   US-09-806-708B-22       Sequence 22, Appl
       5        46       2.0   41736   4   US-09-949-016-17091     Sequence 17091, A
c      6      45.6       1.9   42348   4   US-09-949-016-17157     Sequence 17157, A
       7      45.4       1.9    2327   4   US-10-066-130-20        Sequence 20, Appl
       8      45.4       1.9    2674   4   US-10-066-130-19        Sequence 19, Appl
       9      45.4       1.9    2771   4   US-10-066-130-18        Sequence 18, Appl
      10      45.4       1.9    5860   4   US-10-066-130-17        Sequence 17, Appl
c     11      45.4       1.9   12980   3   US-08-811-566-5         Sequence 5, Appli
c     12      45.4       1.9   12980   3   US-09-034-756-5         Sequence 5, Appli
c     13      44.8       1.9  191433   4   US-09-949-016-16144     Sequence 16144, A
      14      43.8       1.9    1141   4   US-09-806-708B-22       Sequence 22, Appl
      15      43.2       1.8     614   4   US-09-902-540-1318      Sequence 1318, Ap
c     16      42.6       1.8   45716   3   US-08-965-048-5         Sequence 5, Appli
c     17      42.6       1.8   45989   3   US-08-965-048-6         Sequence 6, Appli
      18      42.4       1.8    3275   3   US-09-370-838-151       Sequence 151, App
      19      42.4       1.8    3275   4   US-09-854-133-151       Sequence 151, App
      20      42.2       1.8     291   1   US-07-922-723A-7        Sequence 7, Appli
      21      42.2       1.8     291   1   US-07-799-828C-7        Sequence 7, Appli
      22      42.2       1.8     291   1   US-08-074-275-7         Sequence 7, Appli
      23      42.2       1.8     291   1   US-08-480-366-7         Sequence 7, Appli
      24      42.2       1.8     291   2   US-07-952-277A-7        Sequence 7, Appli
      25      42.2       1.8     612   4   US-09-902-540-1357      Sequence 1357, Ap
c     26      42.2       1.8   63804   4   US-09-949-016-15200     Sequence 15200, A
c     27      41.8       1.8     601   4   US-09-949-016-157832    Sequence 157832,
c     28      41.6       1.8  154023   4   US-09-949-016-17057     Sequence 17057, A
c     29      41.2       1.8     601   4   US-09-949-016-89635     Sequence 89635, A
c     30      41.2       1.8     601   4   US-09-949-016-89636     Sequence 89636, A
      31      41.2       1.8    1447   3   US-09-443-041A-27       Sequence 27, Appl
      32      41.2       1.8    2262   4   US-09-311-021-171       Sequence 171, App
c     33      41.2       1.8   23927   4   US-09-949-016-14284     Sequence 14284, A
c     34        41       1.7     601   4   US-09-949-016-193621    Sequence 193621,
      35        41       1.7     801   4   US-09-792-024-10        Sequence 10, Appl
      36        41       1.7  580073   4   US-08-545-528D-1        Sequence 1, Appli
      37      40.8       1.7    2223   1   US-08-257-073-4         Sequence 4, Appli
      38      40.8       1.7  168174   4   US-10-071-411A-63       Sequence 63, Appl
      39      40.8       1.7  168273   4   US-10-071-411A-2        Sequence 2, Appli
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40    40.6    1.7    2608    4   US-09-904-615-16        Sequence 16, Appl
41    40.4    1.7     240    1   US-08-628-417-6         Sequence 6, Appli
42    40.4    1.7    1696    4   US-09-835-811-1         Sequence 1, Appli
43      40    1.7    1798    3   US-09-797-906-1         Sequence 1, Appli
44      40    1.7   49931    4   US-09-949-016-13727     Sequence 13727, A
45      40    1.7   49931    4   US-09-949-016-13728     Sequence 13728, A
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ALIGNMENTS

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 03:39:00 ; Search time 1330 Seconds
                                             (without alignments)
                                             10671.499 Million cell updates/sec

Title: US-09-771-312-1
Perfect score: 2345
Sequence: 1 attcggcacgaggtggaagt.........accaaaaaaaaaaaaaaaaa 2345

Scoring table: IDENTITY_NUC
                  Gapop 10.0 , Gapext 1.0

Searched: 5607317 seqs, 3026245999 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
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                  2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                  3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                  4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                  5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                  6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                  7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                  8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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                  13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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                  17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
                  18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2345	100.0	2345	11	US-09-771-312-1	Sequence 1, Appli
	2	2314.8	98.7	2583	14	US-10-198-846-13132	Sequence 13132, A
	3	2314.4	98.7	2338	18	US-10-788-792-118	Sequence 118, App
	4	495.4	21.1	733	18	US-10-425-115-116525	Sequence 116525,
	5	467	19.9	467	17	US-10-242-535A-27975	Sequence 27975, A
	6	467	19.9	467	17	US-10-085-783A-27975	Sequence 27975, A
c	7	405.2	17.3	425	11	US-09-771-312-3	Sequence 3, Appli
	8	385.4	16.4	492	14	US-10-198-846-6102	Sequence 6102, Ap
	9	382	16.3	382	10	US-09-822-846-358	Sequence 358, App
c	10	291.2	12.4	360	9	US-09-880-107-2493	Sequence 2493, Ap
	11	250.2	10.7	330	15	US-10-102-524-1155	Sequence 1155, Ap
	12	191.8	8.2	308	17	US-10-242-535A-18279	Sequence 18279, A
	13	191.8	8.2	308	17	US-10-085-783A-18279	Sequence 18279, A
	14	128.6	5.5	418	13	US-10-027-632-284593	Sequence 284593,
	15	128.6	5.5	418	17	US-10-027-632-284593	Sequence 284593,
	16	99.8	4.3	371	10	US-09-764-891-1648	Sequence 1648, Ap
	17	93.4	4.0	171	9	US-09-783-590-5298	Sequence 5298, Ap
	18	64.8	2.8	321	10	US-09-814-353-4307	Sequence 4307, Ap
	19	64.8	2.8	321	10	US-09-814-353-10611	Sequence 10611, A
	20	64.8	2.8	390	10	US-09-814-353-16995	Sequence 16995, A
	21	60	2.6	60	10	US-09-908-975-6516	Sequence 6516, Ap
	22	57.8	2.5	673	9	US-09-864-761-26740	Sequence 26740, A
	23	57.8	2.5	673	16	US-10-029-386-24723	Sequence 24723, A
	24	57.8	2.5	978	9	US-09-864-761-10098	Sequence 10098, A
	25	52.6	2.2	496	17	US-10-424-599-74788	Sequence 74788, A
	26	50	2.1	464	10	US-09-918-995-4057	Sequence 4057, Ap
	27	49.8	2.1	1151	17	US-10-424-599-31742	Sequence 31742, A
	28	49.8	2.1	684187	18	US-10-367-094-71	Sequence 71, Appl
	29	49.6	2.1	373	17	US-10-242-535A-3209	Sequence 3209, Ap
	30	49.6	2.1	373	17	US-10-085-783A-3209	Sequence 3209, Ap
	31	49.6	2.1	2575	10	US-09-960-706-955	Sequence 955, App
	32	49.6	2.1	2575	10	US-09-873-319-624	Sequence 624, App
	33	49.6	2.1	3094	10	US-09-957-763-1	Sequence 1, Appli
	34	49.6	2.1	3094	10	US-09-957-763-3	Sequence 3, Appli
	35	48.6	2.1	627	18	US-10-021-323-9336	Sequence 9336, Ap
c	36	48.4	2.1	417	18	US-10-425-115-158260	Sequence 158260,
	37	48.2	2.1	1629	17	US-10-424-599-9786	Sequence 9786, Ap
c	38	48	2.0	407	18	US-10-437-963-67034	Sequence 67034, A
c	39	48	2.0	247461	18	US-10-322-281-131	Sequence 131, App
	40	47.8	2.0	467	18	US-10-021-323-6541	Sequence 6541, Ap
c	41	47.8	2.0	6668	15	US-10-311-455-1670	Sequence 1670, Ap
	42	47.4	2.0	501	18	US-10-357-930-59111	Sequence 59111, A
	43	47	2.0	2941	14	US-10-198-846-9874	Sequence 9874, Ap

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  44    46.4   2.0  1764  17  US-10-369-022-27          Sequence 27, Appl
  45    46.4   2.0  1764  18  US-10-768-158-15          Sequence 15, Appl
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ALIGNMENTS

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: April 3, 2005, 00:13:53 ; Search time 7542 Seconds
                                             (without alignments)
                                           11835.151 Million cell updates/sec

Title: US-09-771-312-1
Perfect score: 2345
Sequence: 1 attcggcacgaggtggaagt..........accaaaaaaaaaaaaaaaaa 2345

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: gb_est1:*
                 2: gb_est2:*
                 3: gb_htc:*
                 4: gb_est3:*
                 5: gb_est4:*
                 6: gb_est5:*
                 7: gb_est6:*
                 8: gb_gss1:*
                 9: gb_gss2:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES
                      %
Result   Query
   No.   Score   Match Length DB   ID   Description
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     1   1253.8   53.5   2746   3   AK029990   AK029990 Mus muscu
     2   1185.6   50.6   3844   3   AK030026   AK030026 Mus muscu
     3   1055.2   45.0   2234   3   AK053781   AK053781 Mus muscu
```

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| | 4 | 930 | 39.7 | 1099 | 1 | AL539463 | AL539463 AL539463 |
| | 5 | 875.4 | 37.3 | 923 | 5 | BX380890 | BX380890 BX380890 |
| | 6 | 841.4 | 35.9 | 1565 | 3 | AK017975 | AK017975 Mus muscu |
| | 7 | 816.8 | 34.8 | 1961 | 3 | AK032734 | AK032734 Mus muscu |
| | 8 | 780.4 | 33.3 | 816 | 4 | BG210260 | BG210260 RST29795 |
| | 9 | 773.4 | 33.0 | 782 | 5 | BX355142 | BX355142 BX355142 |
| c | 10 | 766.6 | 32.7 | 837 | 5 | BX415499 | BX415499 BX415499 |
| | 11 | 756.2 | 32.2 | 817 | 1 | AU120500 | AU120500 AU120500 |
| | 12 | 755 | 32.2 | 785 | 4 | BG212347 | BG212347 RST31934 |
| | 13 | 752 | 32.1 | 890 | 4 | BG196275 | BG196275 RST15489 |
| | 14 | 746.4 | 31.8 | 770 | 7 | CN365216 | CN365216 170004247 |
| c | 15 | 712 | 30.4 | 895 | 4 | BG189037 | BG189037 RST8073 A |
| c | 16 | 702.6 | 30.0 | 711 | 5 | BQ001706 | BQ001706 UI-H-DH1- |
| c | 17 | 698.6 | 29.8 | 862 | 4 | BG218714 | BG218714 RST38455 |
| | 18 | 696.4 | 29.7 | 702 | 4 | BI766808 | BI766808 603056721 |
| c | 19 | 693 | 29.6 | 696 | 6 | CB528650 | CB528650 UI-H-FT2- |
| c | 20 | 689.8 | 29.4 | 696 | 5 | BM992124 | BM992124 UI-H-DF1- |
| | 21 | 686.4 | 29.3 | 3704 | 3 | AK083471 | AK083471 Mus muscu |
| | 22 | 684.6 | 29.2 | 968 | 4 | BG335967 | BG335967 602404712 |
| | 23 | 678.6 | 28.9 | 790 | 5 | BX415500 | BX415500 BX415500 |
| | 24 | 678 | 28.9 | 678 | 5 | BX955296 | BX955296 DKFZp781N |
| c | 25 | 674 | 28.7 | 694 | 5 | BQ182986 | BQ182986 UI-H-ED1- |
| | 26 | 668.6 | 28.5 | 747 | 4 | BG194707 | BG194707 RST13873 |
| c | 27 | 666.4 | 28.4 | 676 | 4 | BM683630 | BM683630 UI-E-EJ1- |
| | 28 | 661.2 | 28.2 | 667 | 5 | BM929686 | BM929686 UI-E-EJ1- |
| | 29 | 642.8 | 27.4 | 675 | 4 | BI560845 | BI560845 603254011 |
| c | 30 | 642.2 | 27.4 | 659 | 6 | CB046496 | CB046496 NISC_gf04 |
| c | 31 | 633.8 | 27.0 | 849 | 4 | BG190649 | BG190649 RST9723 A |
| c | 32 | 631.6 | 26.9 | 843 | 4 | BG203931 | BG203931 RST23324 |
| | 33 | 631.4 | 26.9 | 647 | 5 | BU951125 | BU951125 io76b05.y |
| | 34 | 620.4 | 26.5 | 638 | 6 | CB554977 | CB554977 MMSP0041_ |
| | 35 | 620.4 | 26.5 | 777 | 2 | BE549223 | BE549223 601078779 |
| | 36 | 612.4 | 26.1 | 660 | 4 | BM721009 | BM721009 UI-E-EO0- |
| c | 37 | 611 | 26.1 | 755 | 4 | BG212348 | BG212348 RST31935 |
| c | 38 | 609.8 | 26.0 | 621 | 2 | AW976618 | AW976618 EST388727 |
| | 39 | 593.2 | 25.3 | 752 | 7 | CN365215 | CN365215 170004240 |
| | 40 | 589.8 | 25.2 | 593 | 5 | BX506191 | BX506191 DKFZp686P |
| | 41 | 576.4 | 24.6 | 600 | 4 | BI712934 | BI712934 id99a12.y |
| | 42 | 573.8 | 24.5 | 760 | 7 | CK460603 | CK460603 930893 MA |
| c | 43 | 572 | 24.4 | 572 | 4 | BI791523 | BI791523 id99a12.x |
| | 44 | 567.2 | 24.2 | 572 | 5 | BP203612 | BP203612 BP203612 |
| | 45 | 563.4 | 24.0 | 583 | 5 | BP349820 | BP349820 BP349820 |

OM protein - protein search, using sw model

Run on:          April  3, 2005, 09:05:51 ; Search time 84 Seconds
                                           (without alignments)
                                           2320.562 Million cell updates/sec


Title:           US-09-771-312-2
Perfect score:   2694
Sequence:        1 MEELVHDLVSALEESSEQAR.........GFPLPKSTSATTTPNAGKSA 504


Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5


Searched:        2105692 seqs, 386760381 residues


Total number of hits satisfying chosen parameters:      2105692


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries


Database :       A_Geneseq_16Dec04:*
                 1:  geneseqp1980s:*
                 2:  geneseqp1990s:*
                 3:  geneseqp2000s:*
                 4:  geneseqp2001s:*
                 5:  geneseqp2002s:*
                 6:  geneseqp2003as:*
                 7:  geneseqp2003bs:*
                 8:  geneseqp2004s:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.


                              SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 2694 | 100.0 | 504 | 4 | AAU06524 | Aau06524 Prostate |
| 2 | 2694 | 100.0 | 528 | 4 | AAB92632 | Aab92632 Human pro |
| 3 | 2694 | 100.0 | 528 | 5 | ABB97288 | Abb97288 Novel hum |
| 4 | 1808 | 67.1 | 376 | 8 | ADR99239 | Adr99239 Hypotheti |
| 5 | 825.5 | 30.6 | 313 | 4 | ABG08002 | Abg08002 Novel hum |
| 6 | 608.5 | 22.6 | 423 | 4 | ABG23408 | Abg23408 Novel hum |
| 7 | 591.5 | 22.0 | 446 | 5 | ABB75706 | Abb75706 Human pho |
| 8 | 588.5 | 21.8 | 482 | 5 | ABP43772 | Abp43772 14 clone |
| 9 | 533.5 | 19.8 | 453 | 5 | ABB97561 | Abb97561 Novel hum |

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10    530.5   19.7    351    4   AAB94662         Aab94662  Human pro
11    530.5   19.7    351    5   ABB97470         Abb97470  Novel hum
12      338   12.5    275    4   AAB92468         Aab92468  Human pro
13    320.5   11.9    223    4   AAM15386         Aam15386  Peptide #
14    320.5   11.9    223    4   ABB34392         Abb34392  Peptide #
15    320.5   11.9    223    4   AAM27874         Aam27874  Peptide #
16    320.5   11.9    223    4   ABB29229         Abb29229  Peptide #
17    320.5   11.9    223    4   AAM67577         Aam67577  Human bon
18    320.5   11.9    223    4   AAM55182         Aam55182  Human bra
19    320.5   11.9    223    4   ABG49223         Abg49223  Human liv
20    320.5   11.9    223    4   AAM03148         Aam03148  Peptide #
21    320.5   11.9    223    5   ABG37168         Abg37168  Human pep
22    320.5   11.9    223    8   ABO59933         Abo59933  Human gen
23    236.5    8.8    123    4   AAM95677         Aam95677  Human rep
24      196    7.3   1038    7   ADC03412         Adc03412  Rice flow
25    167.5    6.2    767    6   ABR53431         Abr53431  Protein s
26    167.5    6.2    767    7   ADK64670         Adk64670  Disease t
27    164.5    6.1    554    3   AAG36165         Aag36165  Arabidops
28    164.5    6.1    652    3   AAG36164         Aag36164  Arabidops
29    164.5    6.1    781    3   AAG36163         Aag36163  Arabidops
30    162.5    6.0    815    5   AAG78388         Aag78388  Human H37
31    162.5    6.0    815    7   AAE38620         Aae38620  Human H37
32    162.5    6.0    815    7   AAE38621         Aae38621  Human H37
33    162.5    6.0    815    8   ADP23184         Adp23184  PRO polyp
34      162    6.0    381    2   AAY07056         Aay07056  Renal can
35    157.5    5.8    852    7   ADD45318         Add45318  Rat Prote
36    157.5    5.8    852    7   ADE56352         Ade56352  Rat Prote
37    156.5    5.8    573    4   ADM19760         Adm19760  Protein e
38      156    5.8    929    4   AAM78604         Aam78604  Human pro
39      156    5.8    930    8   ABM82400         Abm82400  Tumour-as
40      156    5.8   1041    4   AAM79588         Aam79588  Human pro
41      151    5.6    641    3   AAB58944         Aab58944  Breast an
42    148.5    5.5    962    4   ABG04842         Abg04842  Novel hum
43    148.5    5.5   1403    8   ADH09502         Adh09502  Human hos
44    148.5    5.5   1462    6   ABP58346         Abp58346  Human cel
45    148.5    5.5   1462    6   ABU05132         Abu05132  Human exp
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<div align="center">

ALIGNMENTS
GenCore version 5.1.6
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</div>

OM protein - protein search, using sw model

Run on: April 3, 2005, 09:24:37 ; Search time 26 Seconds
                                             (without alignments)
                                             1447.043 Million cell updates/sec

Title: US-09-771-312-2
Perfect score: 2694
Sequence: 1 MEELVHDLVSALEESSEQAR.........GFPLPKSTSATTTPNAGKSA 504

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_AA:*
                  1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                  2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                  3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                  4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                  5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

| | | % Query | | | | |
Result No.	Score	Match	Length	DB	ID	Description
1	534	19.8	124	4	US-09-621-976-4580	Sequence 4580, Ap
2	162.5	6.0	815	4	US-09-538-092-1196	Sequence 1196, Ap
3	156	5.8	929	4	US-09-538-092-1232	Sequence 1232, Ap
4	151.5	5.6	620	4	US-09-270-767-46214	Sequence 46214, A
5	148.5	5.5	1462	4	US-09-538-092-1043	Sequence 1043, Ap
6	147.5	5.5	362	4	US-09-270-767-42306	Sequence 42306, A
7	131.5	4.9	1564	4	US-10-144-198-2	Sequence 2, Appli
8	131.5	4.9	1564	4	US-10-144-198-4	Sequence 4, Appli
9	126.5	4.7	1402	4	US-09-248-796A-14503	Sequence 14503, A
10	126	4.7	598	4	US-09-538-092-1083	Sequence 1083, Ap
11	126	4.7	1400	4	US-09-764-176-7	Sequence 7, Appli
12	124.5	4.6	748	3	US-08-725-459B-24	Sequence 24, Appl
13	122	4.5	664	1	US-08-421-661-6	Sequence 6, Appli
14	120.5	4.5	1034	4	US-09-976-594-590	Sequence 590, App
15	119	4.4	733	3	US-08-725-459B-21	Sequence 21, Appl
16	118.5	4.4	1739	4	US-09-976-594-76	Sequence 76, Appl
17	118.5	4.4	1739	4	US-09-538-092-824	Sequence 824, App
18	118.5	4.4	1740	4	US-09-949-016-8860	Sequence 8860, Ap
19	118	4.4	769	3	US-08-725-459B-39	Sequence 39, Appl
20	117.5	4.4	621	4	US-09-248-796A-15807	Sequence 15807, A
21	117.5	4.4	810	3	US-09-540-824-25	Sequence 25, Appl
22	117.5	4.4	848	4	US-09-248-796A-18403	Sequence 18403, A
23	117	4.3	733	3	US-08-725-459B-22	Sequence 22, Appl
24	117	4.3	769	3	US-08-725-459B-37	Sequence 37, Appl
25	117	4.3	769	3	US-08-725-459B-38	Sequence 38, Appl
26	117	4.3	769	3	US-08-725-459B-40	Sequence 40, Appl
27	116.5	4.3	971	4	US-09-538-092-1332	Sequence 1332, Ap
28	116.5	4.3	1032	4	US-09-976-594-214	Sequence 214, App
29	116.5	4.3	1589	4	US-09-543-681A-4998	Sequence 4998, Ap
30	116.5	4.3	1969	4	US-09-418-710-72	Sequence 72, Appl

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31   116.5    4.3    1969  4  US-09-839-479-71       Sequence 71, Appl
32   116.5    4.3    1972  4  US-09-418-710-21       Sequence 21, Appl
33   116.5    4.3    1972  4  US-09-839-479-21       Sequence 21, Appl
34   116      4.3     473  4  US-09-248-796A-15689   Sequence 15689, A
35   116      4.3     709  4  US-09-949-016-10367    Sequence 10367, A
36   115.5    4.3    1085  1  US-08-431-080-28       Sequence 28, Appl
37   115.5    4.3    1085  2  US-08-938-534-28       Sequence 28, Appl
38   115.5    4.3    1085  3  US-09-345-294-28       Sequence 28, Appl
39   115.5    4.3    2907  4  US-09-698-295-1        Sequence 1, Appli
40   115      4.3     664  4  US-09-917-254-78       Sequence 78, Appl
41   115      4.3     779  4  US-10-164-595-56       Sequence 56, Appl
42   115      4.3     968  3  US-09-302-812-6        Sequence 6, Appli
43   115      4.3     968  3  US-09-511-477-6        Sequence 6, Appli
44   115      4.3     968  3  US-09-511-507-6        Sequence 6, Appli
45   115      4.3    2842  1  US-07-741-940-7        Sequence 7, Appli
```

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OM protein - protein search, using sw model

Run on: April 3, 2005, 09:32:12 ; Search time 74 Seconds
                                              (without alignments)
                                              2258.416 Million cell updates/sec

Title: US-09-771-312-2
Perfect score: 2694
Sequence: 1 MEELVHDLVSALEESSEQAR.........GFPLPKSTSATTTPNAGKSA 504

Scoring table: BLOSUM62
                   Gapop 10.0 , Gapext 0.5

Searched: 1413372 seqs, 331592847 residues

Total number of hits satisfying chosen parameters: 1413372

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_AA:*
                   1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
                   2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                   3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                   4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
                   5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                   6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
                   7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                   8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
                   9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
                   10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
                   11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

```
12:  /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13:  /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14:  /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15:  /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16:  /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17:  /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18:  /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19:  /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20:  /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2694	100.0	504	11	US-09-771-312-2	Sequence 2, Appli
2	1808	67.1	376	16	US-10-788-792-245	Sequence 245, App
3	529	19.6	320	11	US-09-771-312-5	Sequence 5, Appli
4	320.5	11.9	223	9	US-09-864-761-42782	Sequence 42782, A
5	320.5	11.9	223	14	US-10-029-386-33567	Sequence 33567, A
6	236.5	8.8	123	10	US-09-764-891-4335	Sequence 4335, Ap
7	188	7.0	313	15	US-10-424-599-174584	Sequence 174584,
8	181.5	6.7	564	15	US-10-425-114-71576	Sequence 71576, A
9	169	6.3	776	16	US-10-437-963-198660	Sequence 198660,
10	162.5	6.0	815	10	US-09-957-763-2	Sequence 2, Appli
11	162.5	6.0	815	10	US-09-957-763-4	Sequence 4, Appli
12	159	5.9	729	16	US-10-437-963-127682	Sequence 127682,
13	155.5	5.8	150	16	US-10-767-701-33562	Sequence 33562, A
14	151	5.6	641	9	US-09-925-298-652	Sequence 652, App
15	151	5.6	641	14	US-10-102-806-652	Sequence 652, App
16	149	5.5	668	15	US-10-424-599-256096	Sequence 256096,
17	148.5	5.5	1462	14	US-10-287-218-17	Sequence 17, Appl
18	148.5	5.5	1462	16	US-10-408-765A-756	Sequence 756, App
19	148.5	5.5	1462	16	US-10-474-291-17	Sequence 17, Appl
20	145	5.4	1604	16	US-10-437-963-123905	Sequence 123905,
21	143	5.3	1577	15	US-10-369-493-6924	Sequence 6924, Ap
22	143	5.3	1577	15	US-10-369-493-6925	Sequence 6925, Ap
23	143	5.3	1577	15	US-10-369-493-6926	Sequence 6926, Ap
24	140	5.2	198	15	US-10-108-260A-4770	Sequence 4770, Ap
25	138.5	5.1	158	16	US-10-767-701-42233	Sequence 42233, A
26	138	5.1	42	11	US-09-771-312-6	Sequence 6, Appli
27	135.5	5.0	557	9	US-09-764-856-60	Sequence 60, Appl
28	135.5	5.0	557	11	US-09-764-856-60	Sequence 60, Appl
29	135.5	5.0	557	14	US-10-102-627-60	Sequence 60, Appl
30	135.5	5.0	643	15	US-10-427-224-13	Sequence 13, Appl
31	134	5.0	644	16	US-10-437-963-109393	Sequence 109393,
32	133	4.9	446	9	US-09-764-856-70	Sequence 70, Appl
33	133	4.9	446	11	US-09-764-856-70	Sequence 70, Appl
34	133	4.9	446	14	US-10-102-627-70	Sequence 70, Appl
35	131.5	4.9	324	15	US-10-425-114-59181	Sequence 59181, A
36	131.5	4.9	341	15	US-10-424-599-256098	Sequence 256098,
37	131.5	4.9	420	9	US-09-764-868-900	Sequence 900, App
38	131.5	4.9	1564	15	US-10-144-198-2	Sequence 2, Appli

```
39   131.5    4.9   1564  15  US-10-144-198-4             Sequence 4, Appli
40   130.5    4.8   1285   9  US-09-982-091A-2          Sequence 2, Appli
41   130      4.8    616  17  US-10-488-614-1            Sequence 1, Appli
42   130      4.8    616  17  US-10-488-608-1            Sequence 1, Appli
43   130      4.8   1424  16  US-10-437-963-160683       Sequence 160683,
44   129.5    4.8    645  17  US-10-488-614-3            Sequence 3, Appli
45   129.5    4.8    645  17  US-10-488-608-3            Sequence 3, Appli
```

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OM protein - protein search, using sw model

Run on: April 3, 2005, 09:23:11 ; Search time 26 Seconds
                                            (without alignments)
                                            1865.125 Million cell updates/sec

Title: US-09-771-312-2
Perfect score: 2694
Sequence: 1 MEELVHDLVSALEESSEQAR.........GFPLPKSTSATTTPNAGKSA 504

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   PIR_79:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
   No.   Score Match Length DB ID   Description
   ----
      1   177.5   6.6   1105   2 T47582   hypothetical prote
      2   167.5   6.2   767   2 S63182   hypothetical prote
      3   156   5.8   542   2 T46464   hypothetical prote
      4   149   5.5   695   2 T40168   hypothetical prote
```

```
 5   148.5   5.5   1403   1   A47328      natural killer cel
 6   146.5   5.4    669   2   T28754      hypothetical prote
 7   143     5.3   1577   2   T19722      hypothetical prote
 8   143     5.3   3498   2   T22330      hypothetical prote
 9   138.5   5.1    368   2   G88636      protein W09G12.7 [
10   135.5   5.0    643   2   A96636      unknown protein, 7
11   134.5   5.0    699   2   I38073      nucleolar phosphop
12   134.5   5.0    896   2   D96556      hypothetical prote
13   133.5   5.0   1672   2   T46237      hypothetical prote
14   133     4.9    705   2   D88536      acidic protein - C
15   133     4.9    705   2   S27786      acidic protein - C
16   133     4.9    943   2   A42681      centromere protein
17   131.5   4.9    425   2   S55147      hypothetical prote
18   130     4.8    608   2   T02299      hypothetical prote
19   130     4.8    679   2   S48437      hypothetical prote
20   129.5   4.8   2526   2   T20531      hypothetical prote
21   129.5   4.8   2722   2   T20532      hypothetical prote
22   129.5   4.8   2738   2   E88320      protein F07A11.6 [
23   128.5   4.8    543   2   T27190      hypothetical prote
24   128.5   4.8    552   2   T27191      hypothetical prote
25   128.5   4.8    954   2   E86174      protein F19P19.26
26   127.5   4.7    493   2   T02376      hypothetical prote
27   127.5   4.7    539   2   T15256      hypothetical prote
28   127     4.7    763   2   T08929      hypothetical prote
29   127     4.7    786   2   T33856      hypothetical prote
30   127     4.7    845   2   A45669      neurofilament trip
31   127     4.7    963   2   T04002      hypothetical prote
32   126.5   4.7    390   2   T34137      hypothetical prote
33   126     4.7    598   2   B40713      cylicin I - human
34   126     4.7   1032   2   A57514      RNA helicase HEL11
35   125     4.6   1274   2   A89959      hypothetical prote
36   124.5   4.6    817   2   S53919      hypothetical prote
37   124     4.6    775   2   T21259      hypothetical prote
38   124     4.6   1166   2   H86341      hypothetical prote
39   123.5   4.6    849   2   E86306      Similar to tufteli
40   123     4.6    529   2   T50609      hypothetical prote
41   122     4.5    581   2   T22455      hypothetical prote
42   122     4.5    611   2   T22456      hypothetical prote
43   122     4.5    971   2   T24866      hypothetical prote
44   122     4.5   1230   2   T22458      hypothetical prote
45   121     4.5   4910   2   S64942      probable membrane
```

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OM protein - protein search, using sw model

Run on: April 3, 2005, 09:07:06 ; Search time 89 Seconds
                                             (without alignments)
                                             2899.864 Million cell updates/sec

Title: US-09-771-312-2
Perfect score: 2694
Sequence: 1 MEELVHDLVSALEESSEQAR.........GFPLPKSTSATTTPNAGKSA 504

```
Scoring table:   BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched:        1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters:       1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :       UniProt_03:*
                 1:  uniprot_sprot:*
                 2:  uniprot_trembl:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES
                      %
Result           Query
   No.    Score  Match Length DB  ID                    Description
--------------------------------------------------------------------------------
     1     2694  100.0    528  1  GPT2_HUMAN            Q9nw75 homo sapien
     2     2310   85.7    527  1  GPT2_MOUSE            Q7tqc7 mus musculu
     3     1538   57.1    375  2  Q9D3E7                Q9d3e7 mus musculu
     4   1513.5   56.2    410  2  Q6AY15                Q6ay15 rattus norv
     5     1008   37.4    216  2  Q6PIX0                Q6pix0 homo sapien
     6    627.5   23.3    482  2  Q6PE65                Q6pe65 mus musculu
     7    627.5   23.3    500  2  Q6ZPW9                Q6zpw9 mus musculu
     8    593.5   22.0    482  2  Q9H3M3                Q9h3m3 homo sapien
     9      566   21.0    408  2  Q8CD08                Q8cd08 mus musculu
    10      565   21.0    408  2  Q9DA49                Q9da49 mus musculu
    11    533.5   19.8    453  2  Q9NWQ4                Q9nwq4 homo sapien
    12    530.5   19.7    351  2  Q6PEJ7                Q6pej7 homo sapien
    13    530.5   19.7    354  2  Q9ULR8                Q9ulr8 homo sapien
    14      430   16.0    107  2  Q9CSX3                Q9csx3 mus musculu
    15      338   12.5    275  2  Q9NWH0                Q9nwh0 homo sapien
    16    320.5   11.9    221  2  Q9ULA8                Q9ula8 homo sapien
    17      197    7.3    928  2  Q6H4V9                Q6h4v9 oryza sativ
    18    177.5    6.6   1007  2  Q8VYR8                Q8vyr8 arabidopsis
    19    177.5    6.6   1105  2  Q9M383                Q9m383 arabidopsis
    20      170    6.3    812  2  Q6C233                Q6c233 yarrowia li
    21      169    6.3    742  2  Q6Z2C8                Q6z2c8 oryza sativ
    22    167.5    6.2    767  1  YNW4_YEAST            P53866 saccharomyc
    23    164.5    6.1    470  2  Q8CFM0                Q8cfm0 mus musculu
    24    164.5    6.1    663  2  Q80UY8                Q80uy8 mus musculu
    25    164.5    6.1    781  2  Q9SF87                Q9sf87 arabidopsis
    26    163.5    6.1   1067  2  Q8BY32                Q8by32 m mus muscu
    27    162.5    6.0    815  1  RBM5_HUMAN            P52756 homo sapien
    28    162.5    6.0   1067  2  Q8CH09                Q8ch09 mus musculu
    29      162    6.0    520  2  Q99KV9                Q99kv9 mus musculu
```

30	162	6.0	815	2	Q91YE7	Q91ye7 mus musculu
31	160.5	6.0	749	2	Q6DDU9	Q6ddu9 xenopus lae
32	157.5	5.8	808	2	Q6BYP9	Q6byp9 debaryomyce
33	157.5	5.8	852	1	RBMA_RAT	P70501 rattus norv
34	157.5	5.8	853	2	Q8BTP8	Q8btp8 mus musculu
35	157.5	5.8	857	2	Q80U75	Q80u75 mus musculu
36	157.5	5.8	930	2	Q99KG3	Q99kg3 mus musculu
37	156	5.8	542	2	Q9NTB1	Q9ntb1 homo sapien
38	156	5.8	852	2	Q9BTX0	Q9btx0 homo sapien
39	156	5.8	929	1	RBMA_HUMAN	P98175 homo sapien
40	156	5.8	930	2	Q9BTE4	Q9bte4 homo sapien
41	156	5.8	995	2	Q7Z3D7	Q7z3d7 homo sapien
42	152.5	5.7	711	1	VG5Q_MOUSE	Q7tn31 mus musculu
43	151.5	5.6	832	2	Q9VNC4	Q9vnc4 drosophila
44	149.5	5.5	599	2	Q8MLA6	Q8mla6 drosophila
45	149	5.5	695	2	O74363	O74363 schizosacch

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 3, 2005, 09:33:18 ; Search time 6454 Seconds
                                           (without alignments)
                                           3783.921 Million cell updates/sec

Title: US-09-771-312-2
Perfect score: 2694
Sequence: 1 MEELVHDLVSALEESSEQAR.........GFPLPKSTSATTTPNAGKSA 504

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103709_23798/app_query.fasta_1.6
47
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09771312_@CGN_1_1_4200_@runat_01042005_103709_23798 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*

```
      11:    gb_sts:*
      12:    gb_sy:*
      13:    gb_un:*
      14:    gb_vi:*


      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES
                      %
   Result           Query
      No.    Score  Match  Length DB   ID                        Description
   --------------------------------------------------------------------------------
        1    2694   100.0   2338   6   BD155908                  BD155908 Primer fo
        2    2694   100.0   2338   6   AX876032                  AX876032 Sequence
        3    2694   100.0   2338   9   AK001114                  AK001114 Homo sapi
        4    2694   100.0   2344   6   AX405697                  AX405697 Sequence
        5    2694   100.0   2345   6   AX206855                  AX206855 Sequence
        6    2318    86.0   4537  10   BC054810                  BC054810 Mus muscu
        7    1813    67.3   1026   6   CQ720787                  CQ720787 Sequence
        8    1813    67.3   4022   6   BD183390                  BD183390 Novel gen
        9    1808    67.1   3189   9   BC042193                  BC042193 Homo sapi
       10    1807    67.1   3250   9   BC063474                  BC063474 Homo sapi
       11   1513.5   56.2   1392  10   BC079232                  BC079232 Rattus no
 c     12    1229    45.6 135060   9   AL354659                  AL354659 Human DNA
 c     13    1229    45.6 142908   2   AL513172                  AL513172 Homo sapi
       14   1072.5   39.8 180315  10   AC107843                  AC107843 Mus muscu
 c     15   1072.5   39.8 260404  10   AC110033                  AC110033 Mus muscu
       16    1054    39.1    817   6   BD146304                  BD146304 Primer fo
       17    1054    39.1    817   6   AX866242                  AX866242 Sequence
       18    1038    38.5 254644   2   AC136836                  AC136836 Rattus no
       19    1038    38.5 256511   2   AC135040                  AC135040 Rattus no
 c     20    1038    38.5 262721   2   AC106265                  AC106265 Rattus no
       21    1008    37.4    759   9   BC027719                  BC027719 Homo sapi
       22    627.5   23.3   3947  10   BC058256                  BC058256 Mus muscu
       23    627.5   23.3   4311  10   AK129299                  AK129299 Mus muscu
       24    627.5   23.3   4314  10   BC050782                  BC050782 Mus muscu
       25    608     22.6   1021   9   AK024701                  AK024701 Homo sapi
 c     26    566.5   21.0 148801   5   BX004824                  BX004824 Zebrafish
 c     27    566.5   21.0 149784   2   BX005303                  BX005303 Danio rer
       28    563.5   20.9   2434   6   AX405970                  AX405970 Sequence
       29    563.5   20.9   2463   9   AK000696                  AK000696 Homo sapi
       30    544     20.2    407   6   CQ735676                  CQ735676 Sequence
       31    534     19.8    469   6   AR413083                  AR413083 Sequence
       32    534     19.8    469   6   AX969917                  AX969917 Sequence
       33    534     19.8    469   6   BD108636                  BD108636 EST and e
       34    530.5   19.7   1474   6   AX405879                  AX405879 Sequence
       35    530.5   19.7   1485   9   BC058032                  BC058032 Homo sapi
       36    530.5   19.7   2112   6   BD158526                  BD158526 Primer fo
       37    530.5   19.7   2112   6   AX880680                  AX880680 Sequence
       38    530.5   19.7   2112   9   AK023523                  AK023523 Homo sapi
       39    530.5   19.7   6256   9   AB032978                  AB032978 Homo sapi
       40    422     15.7   1490   9   BC038835                  BC038835 Homo sapi
       41    420     15.6    445   6   CQ431223                  CQ431223 Sequence
       42    417     15.5    849   5   CR523866                  CR523866 Gallus ga
 c     43    387     14.4 177654   2   AC025988                  AC025988 Homo sapi
```

```
c  44      387   14.4 178229  2  AC009420              AC009420 Homo sapi
c  45      387   14.4 185148  9  AC096641              AC096641 Homo sapi
```

<div align="center">

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</div>

OM protein – nucleic search, using frame_plus_p2n model

Run on: April 3, 2005, 09:32:47 ; Search time 780 Seconds
                                            (without alignments)
                                            3825.064 Million cell updates/sec

Title: US-09-771-312-2
Perfect score: 2694
Sequence: 1 MEELVHDLVSALEESSEQAR.........GFPLPKSTSATTTPNAGKSA 504

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103709_23788/app_query.fasta_1.6
47
-DB=N_Geneseq_16Dec04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09771312_@CGN_1_1_644_@runat_01042005_103709_23788 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   N_Geneseq_16Dec04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002as:*
                 7: geneseqn2002bs:*

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 8:  geneseqn2003as:*
 9:  geneseqn2003bs:*
10:   geneseqn2003cs:*
11:   geneseqn2003ds:*
12:   geneseqn2004as:*
13:   geneseqn2004bs:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2694	100.0	2338	4	AAH13916	Aah13916 Human cDN
2	2694	100.0	2338	13	ADR99112	Adr99112 Hypotheti
3	2694	100.0	2344	6	ABN59701	Abn59701 Novel hum
4	2694	100.0	2345	5	AAS11663	Aas11663 Prostate
5	2694	100.0	2583	11	ACN91982	Acn91982 Breast ca
6	1495.5	55.5	1563	5	AAS72189	Aas72189 DNA encod
7	1054	39.1	817	4	AAH04312	Aah04312 Human cDN
c 8	967	35.9	553	6	ABT10667	Abt10667 Human bre
9	600	22.3	1656	5	AAS87595	Aas87595 DNA encod
10	591.5	22.0	1823	6	ABL53700	Abl53700 Human pho
11	588.5	21.8	2433	6	ABQ61016	Abq61016 14 clone
12	563.5	20.9	2434	6	ABN59974	Abn59974 Novel hum
13	530.5	19.7	1474	6	ABN59883	Abn59883 Novel hum
14	530.5	19.7	2112	4	AAH16534	Aah16534 Human cDN
15	439	16.3	330	7	ADS72558	Ads72558 Human kid
16	420	15.6	445	4	AAL23787	Aal23787 Human bre
17	420	15.6	492	11	ACN84952	Acn84952 Breast ca
18	377	14.0	448	4	AAL14929	Aal14929 Human bre
19	348.5	12.9	1851	4	AAH13673	Aah13673 Human cDN
20	321.5	11.9	740	4	AAH03286	Aah03286 Human cDN
21	320.5	11.9	673	4	AAI21087	Aai21087 Probe #11
22	320.5	11.9	673	4	ABA66165	Aba66165 Human foe
23	320.5	11.9	673	4	AAI46350	Aai46350 Probe #15
24	320.5	11.9	673	4	ABA48281	Aba48281 Human bre
25	320.5	11.9	673	4	AAK40330	Aak40330 Human bon
26	320.5	11.9	673	4	AAK14584	Aak14584 Human bra
27	320.5	11.9	673	4	ABS39901	Abs39901 Human liv
28	320.5	11.9	673	5	AAI06807	Aai06807 Probe #67
29	320.5	11.9	673	6	ABS14348	Abs14348 Human gen
30	320.5	11.9	673	12	ACH91528	Ach91528 Human gen
31	313	11.6	978	4	AAI11878	Aai11878 Probe #18
32	313	11.6	978	4	ABA53579	Aba53579 Human foe
33	313	11.6	978	4	AAI33206	Aai33206 Probe #18
34	313	11.6	978	4	ABA43160	Aba43160 Human bre
35	313	11.6	978	4	AAK27304	Aak27304 Human bon
36	313	11.6	978	4	AAK01845	Aak01845 Human bra
37	313	11.6	978	4	ABS26879	Abs26879 Human liv
38	313	11.6	978	5	AAI01816	Aai01816 Probe #18
39	313	11.6	978	6	ABS01825	Abs01825 Human gen
40	236.5	8.8	371	4	AAL01647	Aal01647 Human rep
41	232	8.6	464	9	ACH16845	Ach16845 Human adu

42	213.5	7.9	747	2	AAZ16358	Aaz16358 Human gen
43	200.5	7.4	300	2	AAZ14849	Aaz14849 Human gen
44	197	7.3	3117	10	ADC03411	Adc03411 Rice flow
45	189	7.0	382	6	ABK35967	Abk35967 cDNA sequ

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 3, 2005, 09:37:13 ; Search time 255 Seconds
                                          (without alignments)
                                          3234.053 Million cell updates/sec

Title: US-09-771-312-2
Perfect score: 2694
Sequence: 1 MEELVHDLVSALEESSEQAR.........GFPLPKSTSATTTPNAGKSA 504

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103710_23824/app_query.fasta_1.6
47
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09771312_@CGN_1_1_177_@runat_01042005_103710_23824 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	534	19.8	469	4	US-09-621-976-720	Sequence 720, App
c	2	164.5	6.1	1200	4	US-09-270-767-10714	Sequence 10714, A
	3	164.5	6.1	1863	4	US-09-270-767-14647	Sequence 14647, A
c	4	146	5.4	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	5	146	5.4	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	6	136	5.0	2131	4	US-09-270-767-10558	Sequence 10558, A
c	7	134.5	5.0	2132	4	US-09-270-767-12419	Sequence 12419, A
	8	134.5	5.0	6088	4	US-09-620-312D-190	Sequence 190, App
	9	134.5	5.0	6316	4	US-09-976-594-974	Sequence 974, App
	10	134	5.0	6775	4	US-09-620-312D-289	Sequence 289, App
	11	133	4.9	43804	3	US-09-171-461-1	Sequence 1, Appli
	12	133	4.9	43804	4	US-09-970-711-1	Sequence 1, Appli
	13	132	4.9	1307	4	US-09-023-655-293	Sequence 293, App
	14	132	4.9	4209	4	US-09-248-796A-400	Sequence 400, App
	15	131.5	4.9	6429	4	US-10-144-198-3	Sequence 3, Appli
	16	131.5	4.9	6726	4	US-10-144-198-1	Sequence 1, Appli
	17	131	4.9	2040	4	US-09-614-221A-396	Sequence 396, App
	18	128.5	4.8	4773	4	US-09-270-767-14129	Sequence 14129, A
	19	127.5	4.7	1269	4	US-09-489-039A-979	Sequence 979, App
c	20	127.5	4.7	1425	4	US-09-489-039A-1173	Sequence 1173, Ap
c	21	127.5	4.7	4265	3	US-09-061-709-1	Sequence 1, Appli
c	22	127.5	4.7	4265	4	US-09-899-651-1	Sequence 1, Appli
c	23	127.5	4.7	4265	4	US-09-392-714-15	Sequence 15, Appl
c	24	127.5	4.7	4265	4	US-09-270-437D-1	Sequence 1, Appli
c	25	127.5	4.7	109690	4	US-09-949-016-13525	Sequence 13525, A
c	26	126.5	4.7	4031	2	US-08-993-118-1	Sequence 1, Appli
c	27	126.5	4.7	4031	3	US-08-845-528C-1	Sequence 1, Appli
c	28	126.5	4.7	4031	4	US-09-066-281B-1	Sequence 1, Appli
c	29	126.5	4.7	4031	4	US-09-468-433C-1	Sequence 1, Appli
c	30	126.5	4.7	4225	2	US-08-993-118-9	Sequence 9, Appli
c	31	126.5	4.7	4225	3	US-08-845-528C-9	Sequence 9, Appli
c	32	126.5	4.7	4225	4	US-09-066-281B-9	Sequence 9, Appli
c	33	126.5	4.7	4225	4	US-09-468-433C-9	Sequence 9, Appli
	34	126.5	4.7	6755	3	US-08-931-999-4	Sequence 4, Appli
	35	124.5	4.6	6158	4	US-09-799-451-897	Sequence 897, App
	36	124.5	4.6	12658	4	US-08-956-171E-127	Sequence 127, App
	37	124.5	4.6	12658	4	US-08-781-986A-127	Sequence 127, App
	38	124	4.6	6222	4	US-09-774-528-114	Sequence 114, App
	39	123.5	4.6	3238	4	US-09-949-016-740	Sequence 740, App
	40	123.5	4.6	3238	4	US-09-949-016-5546	Sequence 5546, Ap
	41	123.5	4.6	7600	4	US-09-469-211A-1	Sequence 1, Appli
	42	123	4.6	2302	4	US-09-620-312D-915	Sequence 915, App
	43	123	4.6	2443	4	US-09-949-016-1857	Sequence 1857, Ap
	44	122.5	4.5	1800	1	US-08-139-937-11	Sequence 11, Appl
	45	122.5	4.5	1800	5	PCT-US93-11310-11	Sequence 11, Appl

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OM protein - nucleic search, using frame_plus_p2n model

Run on: April 3, 2005, 11:43:19 ; Search time 828 Seconds
                                             (without alignments)
                                             3684.126 Million cell updates/sec

Title: US-09-771-312-2
Perfect score: 2694
Sequence: 1 MEELVHDLVSALEESSEQAR.........GFPLPKSTSATTTPNAGKSA 504

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 5607317 seqs, 3026245999 residues

Total number of hits satisfying chosen parameters: 11214634

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-
Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103711_23911/app_query.fasta_1.6
47
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09771312_@CGN_1_1_697_@runat_01042005_103711_23911
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*

```
11:  /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12:  /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
13:  /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14:  /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15:  /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16:  /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17:  /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18:  /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19:  /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
20:  /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21:  /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22:  /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2694	100.0	2338	18	US-10-788-792-118	Sequence 118, App
2	2694	100.0	2345	11	US-09-771-312-1	Sequence 1, Appli
3	2694	100.0	2583	14	US-10-198-846-13132	Sequence 13132, A
4	874	32.4	733	18	US-10-425-115-116525	Sequence 116525,
5	439	16.3	330	15	US-10-102-524-1155	Sequence 1155, Ap
6	420	15.6	492	14	US-10-198-846-6102	Sequence 6102, Ap
7	374	13.9	467	17	US-10-242-535A-27975	Sequence 27975, A
8	374	13.9	467	17	US-10-085-783A-27975	Sequence 27975, A
9	320.5	11.9	673	9	US-09-864-761-26740	Sequence 26740, A
10	320.5	11.9	673	16	US-10-029-386-24723	Sequence 24723, A
11	313	11.6	978	9	US-09-864-761-10098	Sequence 10098, A
12	236.5	8.8	371	10	US-09-764-891-1648	Sequence 1648, Ap
13	232	8.6	464	10	US-09-918-995-4057	Sequence 4057, Ap
14	189	7.0	382	10	US-09-822-846-358	Sequence 358, App
15	188	7.0	2540	18	US-10-425-115-137446	Sequence 137446,
16	181.5	6.7	1845	17	US-10-425-114-33626	Sequence 33626, A
17	180.5	6.7	1151	17	US-10-424-599-31742	Sequence 31742, A
18	178	6.6	2331	18	US-10-437-963-96177	Sequence 96177, A
19	174.5	6.5	2980	18	US-10-425-115-57818	Sequence 57818, A
20	162.5	6.0	2575	10	US-09-960-706-955	Sequence 955, App
21	162.5	6.0	2575	10	US-09-873-319-624	Sequence 624, App
22	162.5	6.0	3094	10	US-09-957-763-1	Sequence 1, Appli
23	162.5	6.0	3094	10	US-09-957-763-3	Sequence 3, Appli
24	162	6.0	2208	9	US-09-925-298-234	Sequence 234, App
25	162	6.0	2208	14	US-10-102-806-234	Sequence 234, App
26	159	5.9	2714	18	US-10-437-963-25199	Sequence 25199, A
27	155.5	5.8	539	18	US-10-767-701-1998	Sequence 1998, Ap
28	150.5	5.6	1076	18	US-10-425-115-57819	Sequence 57819, A
29	150	5.6	171	9	US-09-783-590-5298	Sequence 5298, Ap
c 30	148.5	5.5	1990	9	US-09-864-761-4529	Sequence 4529, Ap
31	148.5	5.5	7058	16	US-10-287-218-38	Sequence 38, Appl
32	148.5	5.5	7058	18	US-10-474-291-38	Sequence 38, Appl
c 33	146	5.4	1683	9	US-09-712-363-13	Sequence 13, Appl
c 34	145	5.4	4950	18	US-10-437-963-21422	Sequence 21422, A
c 35	144.5	5.4	1655	9	US-09-764-856-38	Sequence 38, Appl

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c  36   144.5   5.4   1655   11   US-09-764-856-38           Sequence 38, Appl
c  37   144.5   5.4   1655   14   US-10-102-627-38           Sequence 38, Appl
c  38   143.5   5.3   1960    9   US-09-864-761-4620      Sequence 4620, Ap
   39   143.5   5.3   3727   15   US-10-171-581-49           Sequence 49, Appl
   40    143    5.3   2995   17   US-10-424-599-113254    Sequence 113254,
   41   142.5   5.3   1938   15   US-10-106-698-1570         Sequence 1570, Ap
   42   142.5   5.3   2272   10   US-09-946-374-307          Sequence 307, App
   43   142.5   5.3   2272   13   US-10-052-586-345          Sequence 345, App
   44   142.5   5.3   2272   14   US-10-174-590-345          Sequence 345, App
   45   142.5   5.3   2272   14   US-10-176-758-345          Sequence 345, App
```

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OM protein – nucleic search, using frame_plus_p2n model

Run on: April 3, 2005, 09:36:48 ; Search time 4719 Seconds
                                            (without alignments)
                                            4065.351 Million cell updates/sec

Title: US-09-771-312-2
Perfect score: 2694
Sequence: 1 MEELVHDLVSALEESSEQAR.........GFPLPKSTSATTTPNAGKSA 504

Scoring table: BLOSUM62
                  Xgapop 10.0 , Xgapext 0.5
                  Ygapop 10.0 , Ygapext 0.5
                  Fgapop 6.0 , Fgapext 7.0
                  Delop   6.0 , Delext   7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US09771312/runat_01042005_103709_23808/app_query.fasta_1.6
47
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09771312_@CGN_1_1_4352_@runat_01042005_103709_23808 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

```
Database :        EST:*
                  1:  gb_est1:*
                  2:  gb_est2:*
                  3:  gb_htc:*
                  4:  gb_est3:*
                  5:  gb_est4:*
                  6:  gb_est5:*
                  7:  gb_est6:*
                  8:  gb_gss1:*
                  9:  gb_gss2:*


         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.
```

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	2301	85.4	3844	3	AK030026	AK030026 Mus muscu
	2	2275	84.4	2746	3	AK029990	AK029990 Mus muscu
	3	2089.5	77.6	2234	3	AK053781	AK053781 Mus muscu
	4	1614	59.9	1961	3	AK032734	AK032734 Mus muscu
	5	1541	57.2	1565	3	AK017975	AK017975 Mus muscu
	6	1389	51.6	1099	1	AL539463	AL539463 AL539463
	7	1338	49.7	770	7	CN365216	CN365216 170004247
	8	1303	48.4	3704	3	AK083471	AK083471 Mus muscu
	9	1209	44.9	968	4	BG335967	BG335967 602404712
	10	1200	44.5	923	5	BX380890	BX380890 BX380890
	11	1179	43.8	790	5	BX415500	BX415500 BX415500
	12	1108	41.1	756	7	CN457551	CN457551 UI-M-HN0-
	13	1100	40.8	782	5	BX355142	BX355142 BX355142
	14	1054	39.1	817	1	AU120500	AU120500 AU120500
	15	1040	38.6	593	5	BX506191	BX506191 DKFZp686P
c	16	1008	37.4	676	4	BM683630	BM683630 UI-E-EJ1-
c	17	998	37.0	659	6	CB046496	CB046496 NISC_gf04
	18	997.5	37.0	716	2	BB654618	BB654618 BB654618
c	19	988	36.7	555	5	BU952562	BU952562 io76b05.x
c	20	988	36.7	560	7	CK820603	CK820603 id99a12.y
c	21	988	36.7	725	1	AJ731509	AJ731509 AJ731509
c	22	984	36.5	572	4	BI791523	BI791523 id99a12.x
	23	983.5	36.5	760	7	CK460603	CK460603 930893 MA
	24	981	36.4	813	7	CK633792	CK633792 UI-M-HN0-
	25	979	36.3	702	4	BI766808	BI766808 603056721
c	26	974	36.2	547	1	AI694727	AI694727 we42c09.x
	27	972	36.1	880	7	CK600754	CK600754 AGENCOURT
	28	968	35.9	678	5	BX955296	BX955296 DKFZp781N
c	29	967	35.9	553	1	AI949698	AI949698 wq13h04.x
c	30	965	35.8	542	2	BE501500	BE501500 hw32h06.x
	31	941	34.9	667	5	BM929686	BM929686 UI-E-EJ1-
	32	919	34.1	638	6	CB554977	CB554977 MMSP0041_
	33	915	34.0	778	7	CO431345	CO431345 UI-M-HX0-
	34	882.5	32.8	791	5	BU480355	BU480355 603842912
	35	881	32.7	675	4	BI560845	BI560845 603254011
	36	872.5	32.4	712	5	BP148863	BP148863 BP148863

	37	860	31.9	717	7	CN535149	CN535149 UI-M-HS0-
c	38	858	31.8	489	1	AI436121	AI436121 ti15f01.y
	39	856	31.8	647	5	BU951125	BU951125 io76b05.y
c	40	837	31.1	536	4	BG063093	BG063093 H3002A11-
c	41	835	31.0	537	4	BG063094	BG063094 H3002A12-
	42	833	30.9	624	1	AJ731494	AJ731494 AJ731494
	43	828.5	30.8	812	7	CR442142	CR442142 CR442142
	44	817	30.3	667	2	BB623181	BB623181 BB623181
	45	810	30.1	633	6	CD349992	CD349992 UI-M-FY0-